



ATTORNEY DOCKET NO. 14014.0323U3

SEQUENCE LISTING

<110> Chiorini, John
Kotin, Robert M.
Safer, Brian

<120> AAV5 VECTOR AND USES THEREOF

<130> 14014.0323U3

<140> 09/717,789

<141> 2000-11-21

<150> PCT/US99/11958

<151> 1999-05-28

<150> 60/087,029

<151> 1998-05-28

<160> 24

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 4652

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 1

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<210> 2
 <211> 390
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 2

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Gln	Trp	Ile	Gln	Glu	Asn	Gln	Glu	Ser	Tyr	Leu	Ser	Phe	Asn	Ser	Thr
			20					25					30		
Gly	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Thr	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Ser	Ala	Val	Asp	Tyr	Leu	Val	Gly	Ser	Ser
	50				55						60				
Val	Pro	Glu	Asp	Ile	Ser	Lys	Asn	Arg	Ile	Trp	Gln	Ile	Phe	Glu	Met
65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Ala	Tyr	Ala	Gly	Ser	Ile	Leu	Tyr	Gly	Trp	Cys
			85						90					95	
Gln	Arg	Ser	Phe	Asn	Lys	Arg	Asn	Thr	Val	Trp	Leu	Tyr	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Asn
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165						170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Val	Gln	Ile	Asp	Ser	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser
		195				200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Lys	Phe
	210				215						220				
Glu	Leu	Thr	Lys	Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Ala	Trp	Ala	Lys	Val	Asn	Gln	Val	Pro	Val
			245						250					255	
Thr	His	Glu	Phe	Lys	Val	Pro	Arg	Glu	Leu	Ala	Gly	Thr	Lys	Gly	Ala
			260					265					270		
Glu	Lys	Ser	Leu	Lys	Arg	Pro	Leu	Gly	Asp	Val	Thr	Asn	Thr	Ser	Tyr
		275				280						285			
Lys	Ser	Leu	Glu	Lys	Arg	Ala	Arg	Leu	Ser	Phe	Val	Pro	Glu	Thr	Pro
	290					295					300				
Arg	Ser	Ser	Asp	Val	Thr	Val	Asp	Pro	Ala	Pro	Leu	Arg	Pro	Leu	Asn
305					310					315					320
Trp	Asn	Ser	Arg	Tyr	Asp	Cys	Lys	Cys	Asp	Tyr	His	Ala	Gln	Phe	Asp
			325						330					335	
Asn	Ile	Ser	Asn	Lys	Cys	Asp	Glu	Cys	Glu	Tyr	Leu	Asn	Arg	Gly	Lys
			340					345					350		
Asn	Gly	Cys	Ile	Cys	His	Asn	Val	Thr	His	Cys	Gln	Ile	Cys	His	Gly
		355				360						365			
Ile	Pro	Pro	Trp	Glu	Lys	Glu	Asn	Leu	Ser	Asp	Phe	Gly	Asp	Phe	Asp
	370					375					380				
Asp	Ala	Asn	Lys	Glu	Gln										
385					390										

ATTORNEY DOCKET NO. 14014.0323U3

<210> 3
 <211> 610
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 3

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Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asp	Trp	Val	Thr	Gly
			20					25					30		
Gln	Ile	Trp	Glu	Leu	Pro	Pro	Glu	Ser	Asp	Leu	Asn	Leu	Thr	Leu	Val
		35					40				45				
Glu	Gln	Pro	Gln	Leu	Thr	Val	Ala	Asp	Arg	Ile	Arg	Arg	Val	Phe	Leu
	50					55					60				
Tyr	Glu	Trp	Asn	Lys	Phe	Ser	Lys	Gln	Glu	Ser	Lys	Phe	Phe	Val	Gln
65				70					75						80
Phe	Glu	Lys	Gly	Ser	Glu	Tyr	Phe	His	Leu	His	Thr	Leu	Val	Glu	Thr
				85					90				95		
Ser	Gly	Ile	Ser	Ser	Met	Val	Leu	Gly	Arg	Tyr	Val	Ser	Gln	Ile	Arg
			100					105					110		
Ala	Gln	Leu	Val	Lys	Val	Val	Phe	Gln	Gly	Ile	Glu	Pro	Gln	Ile	Asn
		115					120					125			
Asp	Trp	Val	Ala	Ile	Thr	Lys	Val	Lys	Lys	Gly	Gly	Ala	Asn	Lys	Val
	130					135					140				
Val	Asp	Ser	Gly	Tyr	Ile	Pro	Ala	Tyr	Leu	Leu	Pro	Lys	Val	Gln	Pro
145					150				155						160
Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Leu	Asp	Glu	Tyr	Lys	Leu	Ala	Ala
			165					170					175		
Leu	Asn	Leu	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	Phe	Leu	Ala	Glu	
		180					185					190			
Ser	Ser	Gln	Arg	Ser	Gln	Glu	Ala	Ala	Ser	Gln	Arg	Glu	Phe	Ser	Ala
	195					200						205			
Asp	Pro	Val	Ile	Lys	Ser	Lys	Thr	Ser	Gln	Lys	Tyr	Met	Ala	Leu	Val
	210					215					220				
Asn	Trp	Leu	Val	Glu	His	Gly	Ile	Thr	Ser	Glu	Lys	Gln	Trp	Ile	Gln
225					230					235					240
Glu	Asn	Gln	Glu	Ser	Tyr	Leu	Ser	Phe	Asn	Ser	Thr	Gly	Asn	Ser	Arg
			245					250					255		
Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Thr	Lys	Ile	Met	Ser	Leu
		260					265						270		
Thr	Lys	Ser	Ala	Val	Asp	Tyr	Leu	Val	Gly	Ser	Ser	Val	Pro	Glu	Asp
	275						280					285			
Ile	Ser	Lys	Asn	Arg	Ile	Trp	Gln	Ile	Phe	Glu	Met	Asn	Gly	Tyr	Asp
	290					295					300				
Pro	Ala	Tyr	Ala	Gly	Ser	Ile	Leu	Tyr	Gly	Trp	Cys	Gln	Arg	Ser	Phe
305					310					315					320
Asn	Lys	Arg	Asn	Thr	Val	Trp	Leu	Tyr	Gly	Pro	Ala	Thr	Thr	Gly	Lys
			325						330					335	
Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	Phe	Tyr	Gly	Cys
		340					345						350		
Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	Cys	Val	Asp	Lys
		355					360					365			
Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Asn	Lys	Val	Val	Glu
	370					375					380				

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Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	Val	Asp	Gln	Lys
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				405					410					415	
Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser	Thr	Thr	Phe	Glu
			420					425					430		
His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Lys	Phe	Glu	Leu	Thr	Lys
		435					440					445			
Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln	Glu	Val	Lys	Asp
	450					455					460				
Phe	Phe	Ala	Trp	Ala	Lys	Val	Asn	Gln	Val	Pro	Val	Thr	His	Glu	Phe
465					470					475					480
Lys	Val	Pro	Arg	Glu	Leu	Ala	Gly	Thr	Lys	Gly	Ala	Glu	Lys	Ser	Leu
				485					490					495	
Lys	Arg	Pro	Leu	Gly	Asp	Val	Thr	Asn	Thr	Ser	Tyr	Lys	Ser	Leu	Glu
			500					505					510		
Lys	Arg	Ala	Arg	Leu	Ser	Phe	Val	Pro	Glu	Thr	Pro	Arg	Ser	Ser	Asp
		515					520					525			
Val	Thr	Val	Asp	Pro	Ala	Pro	Leu	Arg	Pro	Leu	Asn	Trp	Asn	Ser	Arg
	530					535					540				
Tyr	Asp	Cys	Lys	Cys	Asp	Tyr	His	Ala	Gln	Phe	Asp	Asn	Ile	Ser	Asn
545					550					555					560
Lys	Cys	Asp	Glu	Cys	Glu	Tyr	Leu	Asn	Arg	Gly	Lys	Asn	Gly	Cys	Ile
				565					570					575	
Cys	His	Asn	Val	Thr	His	Cys	Gln	Ile	Cys	His	Gly	Ile	Pro	Pro	Trp
			580					585					590		
Glu	Lys	Glu	Asn	Leu	Ser	Asp	Phe	Gly	Asp	Phe	Asp	Asp	Ala	Asn	Lys
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Glu	Gln														
	610														

<210> 4

<211> 724

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 4

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Gly	Leu	Arg	Glu	Phe	Leu	Gly	Leu	Glu	Ala	Gly	Pro	Pro	Lys	Pro	Lys
			20					25					30		
Pro	Asn	Gln	Gln	His	Gln	Asp	Gln	Ala	Arg	Gly	Leu	Val	Leu	Pro	Gly
		35					40					45			
Tyr	Asn	Tyr	Leu	Gly	Pro	Gly	Asn	Gly	Leu	Asp	Arg	Gly	Glu	Pro	Val
	50					55				60					
Asn	Arg	Ala	Asp	Glu	Val	Ala	Arg	Glu	His	Asp	Ile	Ser	Tyr	Asn	Glu
65					70					75					80
Gln	Leu	Glu	Ala	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala	Asp
			85						90					95	
Ala	Glu	Phe	Gln	Glu	Lys	Leu	Ala	Asp	Asp	Thr	Ser	Phe	Gly	Gly	Asn
			100					105					110		
Leu	Gly	Lys	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro	Phe
		115					120					125			
Gly	Leu	Val	Glu	Glu	Gly	Ala	Lys	Thr	Ala	Pro	Thr	Gly	Lys	Arg	Ile
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Asp 145	Asp	His	Phe	Pro	Lys 150	Arg	Lys	Lys	Ala	Arg 155	Thr	Glu	Glu	Asp	Ser 160
Lys	Pro	Ser	Thr	Ser 165	Ser	Asp	Ala	Glu	Ala 170	Gly	Pro	Ser	Gly	Ser	Gln 175
Gln	Leu	Gln	Ile 180	Pro	Ala	Gln	Pro	Ala 185	Ser	Ser	Leu	Gly	Ala	Asp	Thr 190
Met	Ser	Ala 195	Gly	Gly	Gly	Pro 200	Leu	Gly	Asp	Asn 205	Asn	Gln	Gly	Ala	
Asp 210	Gly	Val	Gly	Asn	Ala 215	Ser	Gly	Asp	Trp	His	Cys 220	Asp	Ser	Thr	Trp
Met 225	Gly	Asp	Arg	Val	Val 230	Thr	Lys	Ser	Thr	Arg 235	Thr	Trp	Val	Leu	Pro 240
Ser	Tyr	Asn	Asn 245	His	Gln	Tyr	Arg	Glu	Ile 250	Lys	Ser	Gly	Ser	Val	Asp 255
Gly	Ser	Asn 260	Ala	Asn	Ala	Tyr	Phe	Gly 265	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr 270
Phe	Asp 275	Phe	Asn	Arg	Phe	His 280	Ser	His	Trp	Ser	Pro	Arg	Asp	Trp	Gln 285
Arg 290	Leu	Ile	Asn	Asn	Tyr 295	Trp	Gly	Phe	Arg	Pro	Arg	Ser	Leu	Arg	Val 300
Lys 305	Ile	Phe	Asn	Ile 310	Gln	Val	Lys	Glu	Val	Thr 315	Val	Gln	Asp	Ser	Thr 320
Thr	Thr	Ile	Ala 325	Asn	Asn	Leu	Thr	Ser	Thr 330	Val	Gln	Val	Phe	Thr	Asp 335
Asp	Asp	Tyr 340	Gln	Leu	Pro	Tyr	Val	Val 345	Gly	Asn	Gly	Thr	Glu	Gly	Cys 350
Leu	Pro	Ala 355	Phe	Pro	Pro	Gln	Val	Phe 360	Thr	Leu	Pro	Gln	Tyr	Gly	Tyr 365
Ala 370	Thr	Leu	Asn	Arg	Asp 375	Asn	Thr	Glu	Asn	Pro	Thr	Glu	Arg	Ser	Ser 380
Phe 385	Phe	Cys	Leu	Glu	Tyr 390	Phe	Pro	Ser	Lys	Met 395	Leu	Arg	Thr	Gly	Asn 400
Asn	Phe	Glu	Phe 405	Thr	Tyr	Asn	Phe	Glu	Glu 410	Val	Pro	Phe	His	Ser	Ser 415
Phe	Ala	Pro	Ser 420	Gln	Asn	Leu	Phe	Lys 425	Leu	Ala	Asn	Pro	Leu	Val	Asp 430
Gln	Tyr	Leu 435	Tyr	Arg	Phe	Val	Ser 440	Thr	Asn	Asn	Thr	Gly	Gly	Val	Gln 445
Phe	Asn 450	Lys	Asn	Leu	Ala 455	Gly	Arg	Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp 460
Phe 465	Pro	Gly	Pro	Met	Gly 470	Arg	Thr	Gln	Gly	Trp 475	Asn	Leu	Gly	Ser	Gly 480
Val	Asn	Arg	Ala 485	Ser	Val	Ser	Ala	Phe 490	Ala	Thr	Thr	Asn	Arg	Met	Glu 495
Leu	Glu	Gly	Ala 500	Ser	Tyr	Gln	Val	Pro 505	Pro	Gln	Pro	Asn	Gly	Met	Thr 510
Asn	Asn 515	Leu	Gln	Gly	Ser	Asn	Thr 520	Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile 525
Phe 530	Asn	Ser	Gln	Pro	Ala 535	Asn	Pro	Gly	Thr	Thr	Ala	Thr	Tyr	Leu	Glu 540
Gly 545	Asn	Met	Leu	Ile 550	Thr	Ser	Glu	Ser	Glu	Thr 555	Gln	Pro	Val	Asn	Arg 560
Val	Ala	Tyr	Asn 565	Val	Gly	Gly	Gln	Met	Ala 570	Thr	Asn	Asn	Gln	Ser	Ser 575
Thr	Thr	Ala 580	Pro	Ala	Thr	Gly	Thr	Tyr 585	Asn	Leu	Gln	Glu	Ile	Val	Pro 590
Gly	Ser	Val 595	Trp	Met	Glu	Arg	Asp 600	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp 605
Ala	Lys 610	Ile	Pro	Glu	Thr	Gly	Ala 615	His	Phe	His	Pro	Ser	Pro	Ala	Met 620

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Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	Pro	Pro	Met	Met	Leu	Ile	Lys	Asn
625					630					635					640
Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr	Ser	Phe	Ser	Asp	Val	Pro	Val	Ser
				645					650					655	
Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	Gly	Gln	Val	Thr	Val	Glu	Met	Glu
			660					665					670		
Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln
		675					680					685			
Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	Pro	Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp
	690					695					700				
Ser	Thr	Gly	Glu	Tyr	Arg	Thr	Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu
705					710					715					720
Thr	Arg	Pro	Leu												

<210> 5

<211> 588

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 5

Thr	Ala	Pro	Thr	Gly	Lys	Arg	Ile	Asp	Asp	His	Phe	Pro	Lys	Arg	Lys
1				5				10						15	
Lys	Ala	Arg	Thr	Glu	Glu	Asp	Ser	Lys	Pro	Ser	Thr	Ser	Ser	Asp	Ala
			20					25					30		
Glu	Ala	Gly	Pro	Ser	Gly	Ser	Gln	Gln	Leu	Gln	Ile	Pro	Ala	Gln	Pro
		35					40					45			
Ala	Ser	Ser	Leu	Gly	Ala	Asp	Thr	Met	Ser	Ala	Gly	Gly	Gly	Gly	Pro
	50					55					60				
Leu	Gly	Asp	Asn	Asn	Gln	Gly	Ala	Asp	Gly	Val	Gly	Asn	Ala	Ser	Gly
65				70						75				80	
Asp	Trp	His	Cys	Asp	Ser	Thr	Trp	Met	Gly	Asp	Arg	Val	Val	Thr	Lys
			85					90						95	
Ser	Thr	Arg	Thr	Trp	Val	Leu	Pro	Ser	Tyr	Asn	Asn	His	Gln	Tyr	Arg
			100					105					110		
Glu	Ile	Lys	Ser	Gly	Ser	Val	Asp	Gly	Ser	Asn	Ala	Asn	Ala	Tyr	Phe
		115					120					125			
Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn	Arg	Phe	His	Ser
	130					135						140			
His	Trp	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly
145				150						155				160	
Phe	Arg	Pro	Arg	Ser	Leu	Arg	Val	Lys	Ile	Phe	Asn	Ile	Gln	Val	Lys
				165					170					175	
Glu	Val	Thr	Val	Gln	Asp	Ser	Thr	Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr
			180				185						190		
Ser	Thr	Val	Gln	Val	Phe	Thr	Asp	Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val
		195					200					205			
Val	Gly	Asn	Gly	Thr	Glu	Gly	Cys	Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val
	210					215					220				
Phe	Thr	Leu	Pro	Gln	Tyr	Gly	Tyr	Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr
225				230						235				240	
Glu	Asn	Pro	Thr	Glu	Arg	Ser	Ser	Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro
				245					250					255	
Ser	Lys	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe
			260					265					270		

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Glu	Glu	Val	Pro	Phe	His	Ser	Ser	Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	
		275					280					285				
Lys	Leu	Ala	Asn	Pro	Leu	Val	Asp	Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser	
	290					295					300					
Thr	Asn	Asn	Thr	Gly	Gly	Val	Gln	Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg	
305					310					315					320	
Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp	Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr	
				325					330					335		
Gln	Gly	Trp	Asn	Leu	Gly	Ser	Gly	Val	Asn	Arg	Ala	Ser	Val	Ser	Ala	
			340					345					350			
Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu	Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val	
		355					360					365				
Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr	Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr	
	370					375					380					
Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile	Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro	
385					390					395					400	
Gly	Thr	Thr	Ala	Thr	Tyr	Leu	Glu	Gly	Asn	Met	Leu	Ile	Thr	Ser	Glu	
			405						410					415		
Ser	Glu	Thr	Gln	Pro	Val	Asn	Arg	Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln	
			420					425					430			
Met	Ala	Thr	Asn	Asn	Gln	Ser	Ser	Thr	Thr	Ala	Pro	Ala	Thr	Gly	Thr	
		435					440					445				
Tyr	Asn	Leu	Gln	Glu	Ile	Val	Pro	Gly	Ser	Val	Trp	Met	Glu	Arg	Asp	
	450					455					460					
Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	Glu	Thr	Gly	Ala	
465					470					475					480	
His	Phe	His	Pro	Ser	Pro	Ala	Met	Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	
				485					490					495		
Pro	Pro	Met	Met	Leu	Ile	Lys	Asn	Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr	
			500					505					510			
Ser	Phe	Ser	Asp	Val	Pro	Val	Ser	Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	
		515					520					525				
Gly	Gln	Val	Thr	Val	Glu	Met	Glu	Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser	
		530				535					540					
Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	Pro	
545					550					555					560	
Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp	Ser	Thr	Gly	Glu	Tyr	Arg	Thr	Thr	
				565					570					575		
Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu	Thr	Arg	Pro	Leu					
			580					585								

<210> 6

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 6

Met	Ser	Ala	Gly	Gly	Gly	Gly	Pro	Leu	Gly	Asp	Asn	Asn	Gln	Gly	Ala	
1				5					10				15			
Asp	Gly	Val	Gly	Asn	Ala	Ser	Gly	Asp	Trp	His	Cys	Asp	Ser	Thr	Trp	
			20				25						30			
Met	Gly	Asp	Arg	Val	Val	Thr	Lys	Ser	Thr	Arg	Thr	Trp	Val	Leu	Pro	
		35					40					45				
Ser	Tyr	Asn	Asn	His	Gln	Tyr	Arg	Glu	Ile	Lys	Ser	Gly	Ser	Val	Asp	
50						55					60					

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Gly 65	Ser	Asn	Ala	Asn 70	Ala	Tyr	Phe	Gly	Tyr	Ser 75	Thr	Pro	Trp	Gly	Tyr 80
Phe	Asp	Phe	Asn	Arg 85	Phe	His	Ser	His	Trp 90	Ser	Pro	Arg	Asp	Trp 95	Gln
Arg	Leu	Ile	Asn 100	Asn	Tyr	Trp	Gly	Phe 105	Arg	Pro	Arg	Ser	Leu 110	Arg	Val
Lys	Ile	Phe 115	Asn	Ile	Gln	Val	Lys 120	Glu	Val	Thr	Val	Gln 125	Asp	Ser	Thr
Thr 130	Thr	Ile	Ala	Asn	Asn	Leu 135	Thr	Ser	Thr	Val	Gln 140	Val	Phe	Thr	Asp
Asp 145	Asp	Tyr	Gln	Leu	Pro 150	Tyr	Val	Val	Gly	Asn 155	Gly	Thr	Glu	Gly	Cys 160
Leu	Pro	Ala	Phe	Pro 165	Pro	Gln	Val	Phe	Thr 170	Leu	Pro	Gln	Tyr	Gly 175	Tyr
Ala	Thr	Leu	Asn 180	Arg	Asp	Asn	Thr	Glu	Asn 185	Pro	Thr	Glu	Arg	Ser 190	Ser
Phe	Phe	Cys 195	Leu	Glu	Tyr	Phe	Pro 200	Ser	Lys	Met	Leu	Arg	Thr 205	Gly	Asn
Asn 210	Phe	Glu	Phe	Thr	Tyr	Asn 215	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	Ser
Phe 225	Ala	Pro	Ser	Gln	Asn 230	Leu	Phe	Lys	Leu	Ala 235	Asn	Pro	Leu	Val	Asp 240
Gln	Tyr	Leu	Tyr	Arg 245	Phe	Val	Ser	Thr	Asn 250	Asn	Thr	Gly	Gly	Val 255	Gln
Phe	Asn	Lys	Asn 260	Leu	Ala	Gly	Arg	Tyr	Ala 265	Asn	Thr	Tyr	Lys	Asn 270	Trp
Phe	Pro	Gly	Pro 275	Met	Gly	Arg	Thr	Gln	Gly	Trp	Asn	Leu	Gly	Ser 285	Gly
Val	Asn	Arg	Ala	Ser	Val	Ser	Ala	Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu
Leu 305	Glu	Gly	Ala	Ser	Tyr	Gln	Val	Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr 320
Asn	Asn	Leu	Gln	Gly 325	Ser	Asn	Thr	Tyr	Ala 330	Leu	Glu	Asn	Thr	Met	Ile 335
Phe	Asn	Ser	Gln 340	Pro	Ala	Asn	Pro	Gly	Thr 345	Thr	Ala	Thr	Tyr	Leu 350	Glu
Gly	Asn	Met	Leu 355	Ile	Thr	Ser	Glu	Ser	Glu	Thr	Gln	Pro	Val	Asn	Arg
Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln	Met	Ala	Thr	Asn	Asn	Gln	Ser	Ser
Thr 385	Thr	Ala	Pro	Ala	Thr	Gly	Thr	Tyr	Asn	Leu	Gln	Glu	Ile	Val	Pro 400
Gly	Ser	Val	Trp	Met	Glu	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp 415
Ala	Lys	Ile	Pro	Glu	Thr	Gly	Ala	His	Phe	His	Pro	Ser	Pro	Ala	Met
Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	Pro	Pro	Met	Met	Leu	Ile	Lys	Asn
Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr	Ser	Phe	Ser	Asp	Val	Pro	Val	Ser
Ser 465	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	Gly	Gln	Val	Thr	Val	Glu	Met	Glu 480
Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln
Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	Pro	Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp
Ser	Thr	Gly	Glu	Tyr	Arg	Thr	Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu
Thr	Arg	Pro	Leu												

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<210> 7
 <211> 2307
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 7

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ctgcgaccgc	tcaattggaa	ttcaagtaaa	taaagcgagt	agtcagtgtct	tttgttgatc	120
accctccaga	ttggttggaa	gaagttggtg	aaggtcttcg	cgagtttttg	ggccttgaag	180
cggggcccacc	gaaacaaaaa	cccaatcagc	agcatcaaga	tcaagcccgt	ggtcttgtgc	240
tgcttggtta	taactatctc	ggacccgga	acggtctcga	tcgaggagag	ctgtcaaca	300
gggcagacga	ggtcgcgcga	gagcacgaca	tctcgtacaa	cgagcagctt	gaggcgggag	360
acaaccccta	cctcaagtac	aaccacgcgg	acgccgagtt	tcaggagaag	ctcgccgacg	420
acacatcctt	cgggggaaac	ctcggaaagg	cagtctttca	ggccaagaaa	agggttctcg	480
aaccttttgg	cctggttgaa	gaggggtgcta	agacggcccc	taccggaaag	cggatagacg	540
accactttcc	aaaaagaaaag	aaggctcggg	ccgaagagga	ctccaagcct	tccacctcgt	600
cagacgccga	agctggaccc	agcggatccc	agcagctgca	aatcccagcc	caaccagcct	660
caagtttggg	agctgataca	atgtctgcgg	gaggtggcgg	cccatgtggc	gacaataacc	720
aaggtgccga	tggagtgggc	aatgcctcgg	gagattggca	ttgcgattcc	acgtggatgg	780
gggacagagt	cgtcaccaag	tccaccgga	cctgggtgct	gcccagctac	aacaaccacc	840
agtaccgaga	gatcaaaaag	ggctccgtcg	acggaagcaa	cgccaacgcc	tactttggat	900
acagcacccc	ctgggggtac	tttgacttta	accgcttcca	cagccactgg	agcccccgag	960
actggcaaaag	actcatcaac	aactactggg	gcttcagacc	ccggtccctc	agagtcaaaa	1020
tcttcaacat	tcaagtcaaa	gaggtcacgg	tgcaggactc	caccaccacc	atcgccaaca	1080
acctcacctc	caccgtccaa	gtgtttacgg	acgacgacta	ccagctgccc	tacgtcgtcg	1140
gcaacgggac	cgagggatgc	ctgccggcct	tccctccgca	ggtctttacg	ctgccgcagt	1200
acgggttacgc	gacgctgaac	cgcgacaaca	cagaaaatcc	caccgagagg	agcagcttct	1260
tctgcctaga	gtactttccc	agcaagatgc	tgagaacggg	caacaacttt	gagtttacct	1320
acaactttga	ggaggtgccc	ttccactcca	gcttcgctcc	cagtcagAAC	ctgttcaagc	1380
tggccaaccc	gctgttggtg	cagtacttgt	accgcttcgt	gagcacaaat	aacactggcg	1440
gagtccagtt	caacaagaac	ctggccggga	gatacgccaa	cacctacaaa	aactgggttc	1500
cggggcccat	gggccgaacc	cagggctgga	acctgggctc	cggggtcaac	cgcgccagtg	1560
tcagcgcctt	cgcacgaccc	aataggatgg	agctcgaggg	cgcgagttac	caggtgcccc	1620
cgcagccgaa	cggcatgacc	aacaacctcc	agggcagcaa	cacctatgcc	ctggagaaca	1680
ctatgatctt	caacagccag	ccggcgaaac	cgggcaccac	cgcacgtac	ctcgagggca	1740
acatgctcat	caccagcgag	agcgagacgc	agccggtgaa	cgcgtggcg	tacaacgtcg	1800
gcgggcagat	ggccaccaac	aaccagagct	ccaccactgc	ccccgcgacc	ggcacgtaca	1860
acctccagga	aatcgtgccc	ggcagcgtgt	ggatggagag	ggacgtgtac	ctccaaggac	1920
ccatctgggc	caagatccca	gagacggggg	cgcactttca	cccctctccg	gccatgggcg	1980
gattcggact	caaacaccca	ccgcccata	tgctcatcaa	gaacacgcct	gtgcccgga	2040
atatcaccag	cttctcggac	gtgcccgta	gcagcttcat	caccacgtac	agcacggggc	2100
aggtcacctg	ggagatggag	tgggagctca	agaaggaaaa	ctccaagagg	tggaaaccag	2160
agatccagta	cacaaacaac	tacaacgacc	cccagtttgt	ggactttgcc	ccggacagca	2220
ccggggaata	cagaaccacc	agacctatcg	gaacccgata	ccttaccoga	cccctttaac	2280
ccattcatgt	cgcataccct	caataaaa				2307

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<210> 8
 <211> 2264
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 8

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ctgcgaccgc	tcaattggaa	ttcaagattg	gttggaagaa	gttgggtgaag	gtcttcgcga	120
gtttttgggc	cttgaagcgg	gcccaccgaa	acaaaaaccc	aatcagcagc	atcaagatca	180
agcccggtgg	cttgtgctgc	ctggttataa	ctatctcgg	cccggaaacg	gtctcgatcg	240
aggagagcct	gtcaacagg	cagacgaggt	cgcgcgagag	cacgacatct	cgtacaacga	300
gcagcttgag	gcgggagaca	acccctacct	caagtacaac	cacgcggacg	ccgagtttca	360
ggagaagctc	gccgacgaca	catccttcgg	gggaaacctc	ggaaaggcag	tcttttcaggc	420
caagaaaagg	gttctcgaac	cttttggcct	ggttgaagag	ggtgctaaga	cggcccttac	480
cggaaagcgg	atagacgacc	actttccaaa	aagaaagaag	gctcggaccg	aagaggactc	540
caagccttcc	acctcgtcag	acgccgaagc	tggacccagc	ggatcccagc	agctgcaaat	600
cccagcccaa	ccagcctcaa	gtttgggagc	tgatacaatg	tctgcgggag	gtggcgggccc	660
attgggcgac	aataaccaag	gtgccgatgg	agtgggcaat	gcctcgggag	attggcattg	720
cgattccacg	tgatggggg	acagagtcgt	caccaagtcc	acccgaacct	gggtgctgcc	780
cagctacaac	aaccaccagt	accgagagat	caaaagcggc	tccgtcgacg	gaagcaacgc	840
caacgcctac	tttgataaca	gcaccccttg	gggtactttt	gactttaacc	gcttccacag	900
ccactggagc	ccccgagact	ggcaaagact	catcaacaac	tactggggct	tcagaccccg	960
gtccctcaga	gtcaaaatct	tcaacattca	agtcaaagag	gtcacggtgc	aggactccac	1020
caccaccatc	gccacaaccc	tcacctccac	cgtccaagtg	tttacggacg	acgactacca	1080
gctgccctac	gtcgtcggca	acgggacoga	gggatgcctg	ccggccttcc	ctccgcaggt	1140
ctttacgctg	ccgcagtagc	gttacgcgac	gctgaaccgc	gacaacacag	aaaatccac	1200
cgagaggagc	agcttcttct	gcctagagta	ctttcccagc	aagatgctga	gaacgggcaa	1260
caactttgag	tttacctaca	actttgagga	gggtgcccttc	cactccagct	tcgctcccag	1320
tcagaacctg	ttcaagctgg	ccaaccgcgt	gggtggaccag	tacttgtacc	gcttcgtgag	1380
cacaaataac	actggcggag	tccagttcaa	caagaacctg	gccgggagat	acgccaacac	1440
ctacaaaaac	tggttcccgg	ggcccatggg	ccgaacccag	ggctggaacc	tgggctccgg	1500
ggtcaaccgc	gccagtgtca	gcgccttcgc	cacgaccaat	aggatggagc	tcgagggcgc	1560
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ctatgccctg	gagaacacta	tgatcttcaa	cagccagccg	gcgaacccgg	gcaccaaccg	1680
cacgtacctc	gagggcaaca	tgctcatcac	cagcgagagc	gagacgcagc	cggtgaaccg	1740
cgtggcgtag	aacgtcggcg	ggcagatggc	caccaacaac	cagagctcca	ccactgcccc	1800
cgcgaccggc	acgtacaacc	tccaggaaat	cgtgcccggc	agcgtgtgga	tggagaggga	1860
cgtgtacctc	caaggaccca	tctgggccaa	gatcccagag	acgggggcgc	actttcaccc	1920
ctctccggcc	atgggcggat	tcggactcaa	acaccaccg	cccatgatgc	tcatacaaga	1980
cacgcctgtg	cccggaataa	tcaccagctt	ctcggacgtg	cccgtcagca	gcttcatcac	2040
ccagtacagc	accgggcagg	tcaccgtgga	gatggagtgg	gagctcaaga	aggaaaactc	2100
caagaggctg	aaccagagag	tccagtacac	aaacaactac	aacgaccccc	agtttgtgga	2160
ctttgccccg	gacagcaccg	gggaatacac	aaccaccaga	cctatcggaa	cccgatacct	2220
taccgcacc	ctttaaccga	ttcatgtcgc	ataccctcaa	taaa		2264

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<210> 9
 <211> 2264
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 9

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gtttttgggc	cttgaagcgg	gccccaccga	acaaaaaccc	aatcagcagc	atcaagatca	180
agcccggtgt	cttgtgctgc	ctggttataa	ctatctcggg	cccggaaacg	gtctcgatcg	240
aggagagcct	gtcaacaggg	cagacgaggt	cgcgcgagag	cacgacatct	cgtacaacga	300
gcagcttgag	gcgggagaca	acccctacct	caagtacaac	cacgcggacg	ccgagtttca	360
ggagaagctc	gccgacgaca	catccttcgg	gggaaacctc	ggaaaggcag	tcttttcaggc	420
caagaaaagg	gttctcgaac	ctttttggcct	ggttgaagag	ggtgctaaga	cggccccctac	480
cggaaagcgg	atagacgacc	actttccaaa	aagaaagaag	gctcggaccg	aagaggactc	540
caagccttcc	acctcgtcag	acgocgaagc	tggacccagc	ggatcccagc	agctgcaaat	600
cccagcccaa	ccagcctcaa	gtttgggagc	tgatacaatg	tctgcgggag	gtggcgggccc	660
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cgattccacg	tgatgggggg	acagagtcgt	caccaagtc	acccgaacct	gggtgctgcc	780
cagctacaac	aaccaccagt	accgagagat	caaaagcggc	tccgtcgacg	gaagcaacgc	840
caacgcctac	tttggtatata	gcacccccctg	gggttacttt	gactttaacc	gcttccacag	900
ccactggagc	ccccgagact	ggcaaagact	catcaacaac	tactggggct	tcagacccccg	960
gtccctcaga	gtcaaaaatct	tcaacattca	agtcaaagag	gtcacgggtg	aggactccac	1020
caccaccatc	gccacaaccc	tcacctccac	cgtccaagtg	tttacggacg	acgactacca	1080
gctgccttac	ctcgtcggca	acgggaccca	gggatgcctg	cgggccttcc	ctccgcaggt	1140
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cgagaggagc	agcttcttct	gcctagagta	ctttcccagc	aagatgctga	gaacgggcaa	1260
caactttgag	tttacctaca	actttgagga	ggtgcccttc	cactccagct	tcgctcccag	1320
tcagaacctg	ttcaagctgg	ccaaccgcgt	ggtggaccag	tacttgtacc	gcttcgtgag	1380
cacaaataac	actggcggag	tccagttcaa	caagaacctg	gccgggagat	acgccaacac	1440
ctacaaaaac	tggttcccgg	ggcccatggg	ccgaacccag	ggctggaacc	tgggctccgg	1500
ggtcaaccgc	gccagtgtca	gcgccttcgc	cacgaccaat	aggatggagc	tcgagggcgc	1560
gagttaccag	gtgccccgcg	agccgaacgg	catgaccaac	aacctccagg	gcagcaacac	1620
ctatgccctg	gagaacacta	tgatcttcaa	cagccagccg	gcgaacccgg	gcaccaaccg	1680
cacgtacctc	gagggcaaca	tgctcatcac	cagcgagagc	gagacgcagc	cggtgaaccg	1740
cgtggcgtac	aacgtcggcg	ggcagatggc	caccaacaac	cagagctcca	ccactgcccc	1800
cgcgaccggc	acgtacaacc	tccaggaaat	cgtgcccggc	agcgtgtgga	tggagagggga	1860
cgtgtacctc	caaggaccca	tctgggcca	gatcccagag	acggggggcg	actttcacc	1920
ctctccggcc	atgggcggat	tcggactcaa	acaccaccg	cccatgatgc	tcatacaaga	1980
cacgcctgtg	cccggaata	tcaccagctt	ctcggacgtg	cccgtcagca	gcttcatcac	2040
ccagtacagc	accgggcagg	tcaccgtgga	gatggagtgg	gagctcaaga	aggaaaactc	2100
caagaggtgg	aaccagagag	tccagtacac	aaacaactac	aacgaccccc	agtttgtgga	2160
ctttgccccg	gacagcaccg	gggaatacag	aaccaccaga	cctatcggaa	cccgatacct	2220
taccgcgacc	ctttaaccga	ttcatgtcgc	ataccctcaa	taaa		2264

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<210> 10
 <211> 1292
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 10

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cttcgcagcg	tgagttctcg	gctgaccogg	tcatcaaaag	caagacttcc	cagaaataca	120
tggcgctcgt	caactggctc	gtggagcacg	gcatacattc	cgagaagcag	tggatccagg	180
aaaatcagga	gagctacctc	tccttcaact	ccaccggcaa	ctctcggagc	cagatcaagg	240
ccgcgctcga	caacgcgacc	aaaattatga	gtctgacaaa	aagcgcggtg	gactacctcg	300
tggggagctc	cgttcccagc	gacattttcaa	aaaacagaat	ctggcaaatt	tttgagatga	360
atgggtacga	cccgccctac	gcgggatcca	tcctctacgg	ctgggtgcag	cgctccttca	420
acaagaggaa	caccgtctgg	ctctacggac	ccgccacgac	cggcaagacc	aacatcgcg	480
aggccatcgc	ccacactgtg	cccttttacg	gctgcgtgaa	ctggaccaat	gaaaactttc	540
cctttaatga	ctgtgtggac	aaaatgctca	tttggtggga	ggagggaaag	atgaccaaca	600
agggtggttga	atccgccaaag	gccatcctgg	ggggctcaaa	ggtgcgggtc	gatcagaaat	660
gtaaatcctc	tgttcaaatt	gattctaccc	ctgtcattgt	aacttccaat	acaaacatgt	720
gtgtggtggt	ggatgggaat	tccacgacct	ttgaacacca	gcagccgctg	gaggaccgca	780
tgttcaaatt	tgaactgact	aagcggctcc	cgccagattt	tggcaagatt	actaagcagg	840
aagtcaagga	cttttttgct	tgggcaaagg	tcaatcaggt	gccggtgact	cacgagttta	900
aagttcccag	ggaattggcg	ggaactaaag	gggaggagaa	atctctaaaa	cgcccactgg	960
gtgacgtcac	caatactagc	tataaaagtc	tggagaagcg	ggccaggctc	tcatattgtc	1020
ccgagacgcc	tcgcagttca	gacgtgactg	ttgatccgcg	tcctctgcga	ccgctcaatt	1080
ggaattcaag	gtatgattgc	aaatgtgact	atcatgctca	atttgacaac	atttctaaca	1140
aatgtgatga	atgtgaatat	ttgaatcggg	gcaaaaatgg	atgtatctgt	cacaatgtaa	1200
ctcactgtca	aatttgtcat	gggattcccc	cctgggaaaa	ggaaaacttg	tcagattttg	1260
gggattttga	cgatgccaat	aaagaacagt	aa			1292

<210> 11
 <211> 1870
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 11

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tgttcgcgtc	ccatttgacg	tggaggaaca	tctgcctgga	atttctgaca	gctttgtgga	120
ctgggtaact	ggtcaaattt	gggagctgcc	tccagagtca	gatttaaatt	tgactctggt	180
tgaacagcct	cagttgacgg	tggctgatag	aattcgccgc	gtgttcctgt	acgagtgga	240
caaatatttc	aagcaggagt	ccaaattctt	tgtgcagttt	gaaaagggat	ctgaatatatt	300
tcactctcac	acgcttgtgg	agacctccgg	catctcttcc	atggtcctcg	gccgctacgt	360
gagtcagatt	cgcgccagc	tggtgaaagt	ggtcttccag	ggaattgaac	cccagatcaa	420
cgactgggtc	gccatcacca	aggtaaagaa	gggaggagcc	aataaggtgg	tggattctgy	480
gtatattccc	gcctacctgc	tggcgaaggt	ccaaccggag	cttcagtggg	cgtggacaaa	540
cctggacgag	tataaattgg	ccgccctgaa	tctggaggag	cgcaaacggc	tcgtcgcgca	600
gtttctggca	gaatcctcgc	agcgtctcga	ggaggcggct	tcgcagcgtg	agttctcggc	660
tgaccgggtc	atcaaaagca	agacttccca	gaaatacatg	gcgctcgta	actggctcgt	720
ggagcacggc	atcacttccg	agaagcagtg	gatccaggaa	aatcaggaga	gctacctctc	780
cttcaactcc	accggcaact	ctcggagcca	gatcaaggcc	gcgctcgaca	acgcgaccaa	840
aattatgagt	ctgacaaaaa	gcgcgggtgga	ctacctcgtg	gggagctccg	ttcccaggga	900
catttcaaaa	aacagaatct	ggcaaatatt	tgagatgaat	ggctacgacc	cggcctacgc	960

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gggatccatc	ctctacggct	ggtgtcagcg	ctccttcaac	aagaggaaca	ccgtctggct	1020
ctacggaccc	gccacgaccg	gcaagaccaa	catcgcgag	gccatcgccc	acactgtgcc	1080
cttttacggc	tgcgtgaact	ggaccaatga	aaactttccc	tttaatgact	gtgtggacaa	1140
aatgtctcatt	tgggtgggag	agggaaagat	gaccaacaag	gtggttgaat	ccgccaaggc	1200
catcctgggg	ggctcaaagg	tgcgggtcga	tcagaaatgt	aaatcctctg	ttcaaattga	1260
ttctacccct	gtcattgtaa	cttccaatac	aaacatgtgt	gtggtggtgg	atgggaattc	1320
cacgaccttt	gaacaccagc	agccgctgga	ggaccgcatg	ttcaaatttg	aactgactaa	1380
gcggtctccg	ccagattttg	gcaagattac	taagcaggaa	gtcaaggact	tttttgcttg	1440
ggcaaaggtc	aatcaggtgc	cggtgactca	cgagtttaaa	gttcccaggg	aattggcggg	1500
aactaaaggg	gcggagaaat	ctctaaaacg	cccactgggt	gacgtcacca	atactagcta	1560
taaaagtctg	gagaagcggg	ccaggctctc	atttgttccc	gagacgcctc	gcagttcaga	1620
cgtgactgtt	gatcccgctc	ctctgcgacc	gctcaattgg	aattcaagg	atgattgcaa	1680
atgtgactat	catgtcfaat	ttgacaacat	ttctaacaaa	tgtgatgaat	gtgaatatatt	1740
gaatcggggc	aaaaatggat	gtatctgtca	caatgtaact	cactgtcaaa	tttgtcatgg	1800
gattccccc	tgggaaaagg	aaaacttgtc	agattttggg	gattttgacg	atgccaaata	1860
agaacagtaa						1870

<210> 12
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 12

Met	Ala	Leu	Val	Asn	Trp	Leu	Val	Glu	His	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asn	Gln	Glu	Ser	Tyr	Leu	Ser	Phe	Asn	Ser	Thr
		20						25					30		
Gly	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Thr	Lys
	35						40					45			
Ile	Met	Ser	Leu	Thr	Lys	Ser	Ala	Val	Asp	Tyr	Leu	Val	Gly	Ser	Ser
	50				55						60				
Val	Pro	Glu	Asp	Ile	Ser	Lys	Asn	Arg	Ile	Trp	Gln	Ile	Phe	Glu	Met
65				70					75					80	
Asn	Gly	Tyr	Asp	Pro	Ala	Tyr	Ala	Gly	Ser	Ile	Leu	Tyr	Gly	Trp	Cys
			85					90						95	
Gln	Arg	Ser	Phe	Asn	Lys	Arg	Asn	Thr	Val	Trp	Leu	Tyr	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Asn
145				150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165					170						175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Val	Gln	Ile	Asp	Ser	Thr	Pro	Val
		180						185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser
		195				200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Lys	Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln
225					230					235				240	
Glu	Val	Lys	Asp	Phe	Phe	Ala	Trp	Ala	Lys	Val	Asn	Gln	Val	Pro	Val
			245					250						255	

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Thr	His	Glu	Phe	Lys	Val	Pro	Arg	Glu	Leu	Ala	Gly	Thr	Lys	Gly	Ala
			260					265					270		
Glu	Lys	Ser	Leu	Lys	Arg	Pro	Leu	Gly	Asp	Val	Thr	Asn	Thr	Ser	Tyr
		275					280					285			
Lys	Ser	Leu	Glu	Lys	Arg	Ala	Arg	Leu	Ser	Phe	Val	Pro	Glu	Thr	Pro
		290				295					300				
Arg	Ser	Ser	Asp	Val	Thr	Val	Asp	Pro	Ala	Pro	Leu	Arg	Pro	Leu	Asn
305					310				315						320
Trp	Asn	Ser	Arg	Leu	Val	Gly	Arg	Ser	Trp						
				325					330						

<210> 13
 <211> 1115
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 13

aggagcgcaa	acggctcgtc	gcgcagtttc	tggcagaatc	ctcgcagcgc	tcgcaggagg	60
cggcttcgca	gcgtgagttc	tcggctgacc	cggatcatcaa	aagcaagact	tcccagaaat	120
acatggcgct	cgtcaactgg	ctcgtggagc	acggcatcac	ttccgagaag	cagtggatcc	180
aggaaaatca	ggagagctac	ctctccttca	actccaccgg	caactctcgg	agccagatca	240
aggccgcgct	cgacaacgcg	acaaaaatta	tgagtctgac	aaaaagcgcg	gtggactacc	300
tcgtggggag	ctccgttccc	gaggacattt	caaaaaacag	aatctggcaa	atttttgaga	360
tgaatggcta	cgaccgggcc	tacgcgggat	ccatectcta	cggctgggtg	cagcgcctct	420
tcaacaagag	gaacaccgtc	tggctctacg	gaccggccac	gaccggcaag	accaacatcg	480
cggaggccat	cgcccacact	gtgccctttt	acggctgcgt	gaactggacc	aatgaaaact	540
ttccctttta	tgactgtgtg	gacaaaatgc	tcatttggtg	ggaggaggga	aagatgacca	600
acaaggtggt	tgaatccgcc	aaggccatcc	tggggggctc	aaaggtgcgg	gtcgatcaga	660
aatgtaaatc	ctctgttcaa	attgattcta	cccctgtcat	tgtaaacttc	aatacaaaaca	720
tgtgtgtggt	ggtggatggg	aattccaaga	cctttgaaca	ccagcagccg	ctggaggacc	780
gcatgttcaa	atttgaactg	actaagcggc	tcccggcaga	ttttggcaag	attactaagc	840
aggaagtcaa	ggactttttt	gcttgggcaa	aggtcaatca	ggtgccggtg	actcacgagt	900
ttaaagttcc	cagggaattg	gcgggaacta	aaggggcgga	gaaatctcta	aaacgcccac	960
tgggtgacgt	caccaatact	agctataaaa	gtctggagaa	gcggggcagg	ctctcatttg	1020
ttcccagagc	gcctcgcagt	tcagacgtga	ctgttgatcc	cgctcctctg	cgaccgcgtca	1080
attggaattc	aagattgggt	ggaagaagtt	ggtga			1115

<210> 14
 <211> 550
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 14

Met	Ala	Thr	Phe	Tyr	Glu	Val	Ile	Val	Arg	Val	Pro	Phe	Asp	Val	Glu
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asp	Trp	Val	Thr	Gly
			20					25				30			
Gln	Ile	Trp	Glu	Leu	Pro	Pro	Glu	Ser	Asp	Leu	Asn	Leu	Thr	Leu	Val
		35					40					45			

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Glu	Gln	Pro	Gln	Leu	Thr	Val	Ala	Asp	Arg	Ile	Arg	Arg	Val	Phe	Leu
50						55					60				
Tyr	Glu	Trp	Asn	Lys	Phe	Ser	Lys	Gln	Glu	Ser	Lys	Phe	Phe	Val	Gln
65					70					75					80
Phe	Glu	Lys	Gly	Ser	Glu	Tyr	Phe	His	Leu	His	Thr	Leu	Val	Glu	Thr
				85					90					95	
Ser	Gly	Ile	Ser	Ser	Met	Val	Leu	Gly	Arg	Tyr	Val	Ser	Gln	Ile	Arg
			100					105					110		
Ala	Gln	Leu	Val	Lys	Val	Val	Phe	Gln	Gly	Ile	Glu	Pro	Gln	Ile	Asn
			115				120					125			
Asp	Trp	Val	Ala	Ile	Thr	Lys	Val	Lys	Lys	Gly	Gly	Ala	Asn	Lys	Val
						135					140				
Val	Asp	Ser	Gly	Tyr	Ile	Pro	Ala	Tyr	Leu	Leu	Pro	Lys	Val	Gln	Pro
145					150					155					160
Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Leu	Asp	Glu	Tyr	Lys	Leu	Ala	Ala
				165				170						175	
Leu	Asn	Leu	Glu	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	Phe	Leu	Ala	Glu
			180					185					190		
Ser	Ser	Gln	Arg	Ser	Gln	Glu	Ala	Ala	Ser	Gln	Arg	Glu	Phe	Ser	Ala
			195				200					205			
Asp	Pro	Val	Ile	Lys	Ser	Lys	Thr	Ser	Gln	Lys	Tyr	Met	Ala	Leu	Val
						215					220				
Asn	Trp	Leu	Val	Glu	His	Gly	Ile	Thr	Ser	Glu	Lys	Gln	Trp	Ile	Gln
225					230					235					240
Glu	Asn	Gln	Glu	Ser	Tyr	Leu	Ser	Phe	Asn	Ser	Thr	Gly	Asn	Ser	Arg
				245					250					255	
Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Thr	Lys	Ile	Met	Ser	Leu
			260					265					270		
Thr	Lys	Ser	Ala	Val	Asp	Tyr	Leu	Val	Gly	Ser	Ser	Val	Pro	Glu	Asp
			275				280					285			
Ile	Ser	Lys	Asn	Arg	Ile	Trp	Gln	Ile	Phe	Glu	Met	Asn	Gly	Tyr	Asp
					295						300				
Pro	Ala	Tyr	Ala	Gly	Ser	Ile	Leu	Tyr	Gly	Trp	Cys	Gln	Arg	Ser	Phe
305					310					315					320
Asn	Lys	Arg	Asn	Thr	Val	Trp	Leu	Tyr	Gly	Pro	Ala	Thr	Thr	Gly	Lys
				325					330					335	
Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	Phe	Tyr	Gly	Cys
			340					345					350		
Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	Cys	Val	Asp	Lys
			355				360					365			
Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Asn	Lys	Val	Val	Glu
					375						380				
Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	Val	Asp	Gln	Lys
385					390					395					400
Cys	Lys	Ser	Ser	Val	Gln	Ile	Asp	Ser	Thr	Pro	Val	Ile	Val	Thr	Ser
				405					410					415	
Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser	Thr	Thr	Phe	Glu
			420					425					430		
His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Lys	Phe	Glu	Leu	Thr	Lys
			435				440					445			
Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln	Glu	Val	Lys	Asp
						455					460				
Phe	Phe	Ala	Trp	Ala	Lys	Val	Asn	Gln	Val	Pro	Val	Thr	His	Glu	Phe
465					470					475					480
Lys	Val	Pro	Arg	Glu	Leu	Ala	Gly	Thr	Lys	Gly	Ala	Glu	Lys	Ser	Leu
				485				490						495	
Lys	Arg	Pro	Leu	Gly	Asp	Val	Thr	Asn	Thr	Ser	Tyr	Lys	Ser	Leu	Glu
			500					505					510		
Lys	Arg	Ala	Arg	Leu	Ser	Phe	Val	Pro	Glu	Thr	Pro	Arg	Ser	Ser	Asp
			515				520					525			

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Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn Trp Asn Ser Arg
 530 535 540
 Leu Val Gly Arg Ser Trp
 545 550

<210> 15
 <211> 1690
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 15

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ctgggtaact	ggtcaaat	gggagctgcc	tccagagtca	gatttaaatt	tgactctggt	180
tgaacagcct	cagttgacgg	tggctgatag	aattcgccgc	gtgttctctgt	acgagtgga	240
caaattttcc	aagcaggagt	ccaaattctt	tgtgcagttt	gaaaagggat	ctgaatat	300
tcatctgcac	acgcttggtg	agacctccgg	catctcttcc	atggctctcg	gccgctacgt	360
gagtcagatt	cgcgccacg	tggtgaaagt	ggtcttccag	ggaattgaac	cccagatcaa	420
cgactgggtc	gcatcacca	aggtaaagaa	gggcgagacc	aataagggtg	tggattctgg	480
gtatattccc	gcctacctgc	tgcgaagggt	ccaaccggag	cttcagtggg	cgtggacaaa	540
cctggacgag	tataaattgg	ccgccctgaa	tctggaggag	cgcaaacggc	tcgtcgcgca	600
gtttctggca	gaatcctcgc	agcgctcgca	ggaggcggct	tcgcagcggtg	agttctcggc	660
tgaccgggtc	atcaaaagca	agacttccca	gaaatacatg	gcgctcgtca	actggctcgt	720
ggagcacggc	atcacttccg	agaagcagtg	gatccaggaa	aatcaggaga	gctacctctc	780
cttcaactcc	accggcaact	ctcggagcca	gatcaaggcc	gcgctcgaca	acgcgaccaa	840
aattatgagt	ctgacaaaaa	gcgcggtgga	ctacctcgtg	gggagctccg	ttcccaggga	900
catttcaaaa	aacagaatct	ggcaaat	tgagatgaat	ggctacgacc	cggcctacgc	960
gggatccatc	ctctacggct	ggtgtcagcg	ctccttcaac	aagaggaaca	ccgtctggct	1020
ctacggaccc	gccacgaccg	gcaagaccaa	catcgcgag	gccatcgccc	acactgtgcc	1080
cttttacggc	tgctgtaact	ggaccaatga	aaactttccc	tttaatgact	gtgtggacaa	1140
aatgctcatt	tggtgggagg	agggaaagat	gaccaacaag	gtggttgaat	ccgccaaaggc	1200
catcctgggg	ggctcaaaag	tgcgggtcga	tcagaaatgt	aaatcctctg	ttcaaattga	1260
ttctaccctt	gtcattgtaa	cttccaatac	aaacatgtgt	gtggtggtgg	atgggaattc	1320
cacgaccttt	gaacaccagc	agccgctgga	ggaccgcatg	ttcaaatttg	aactgactaa	1380
gcggctcccc	ccagattttg	gcaagattac	taagcaggaa	gtcaaggact	tttttgcttg	1440
ggcaaagggtc	aatcaggtgc	cggtgactca	cgagtttaaa	gttcccagg	aattggcggg	1500
aactaaaggg	gcggagaaat	ctctaaaacg	cccactgggt	gacgtcacca	atactagcta	1560
taaaagtctg	gagaagcggg	ccaggctctc	attgttccc	gagacgcctc	gcagttcaga	1620
cgtgactgtt	gatccgctc	ctctgcgacc	gctcaattgg	aattcaagat	tggttggaag	1680
aagttggtga						1690

<210> 16
 <211> 145
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 16

ccatcaccaa	ggtaaagaag	ggcggagcca	ataaggtggt	ggattctggg	tatattcccg	60
cctacctgct	gccgaaggct	caaccggagc	ttcagtgggc	gtggacaaac	ctggacgagt	120
ataaattggc	cgccctgaat	ctgga				145

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<210> 17
<211> 174
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 17

taagcaggaa gtcaaggact tttttgcttg ggcaaaggtc aatcagggtgc cggtgactca	60
cgagttttaa gttcccaggg aattggcggg aactaaaggg gcggagaaat ctctaaaacg	120
cccactgggt gacgtcacca atactagcta taaaagtctg gagaagcggg ccag	174

<210> 18
<211> 187
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 18

cactctcaag caaggggggt ttgtaagcag tgatgtcata atgatgtaat gcttattgtc	60
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cgtatgagtt ctgcgcgagac ttccggggta taaaagaccg agtgaacgag cccgccgcca	180
ttctttg	187

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 19

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cccaaacgag ccagcgagcg agcgaacgag acagggggga gagggtcca	168

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<210> 20
<211> 168
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 20

aaacctcctt gcttgagagt gtggcactct cccccctgtc gcgttcgctc gctcgctggc	60
tcgttttgggg gggcgacggc cagagggccg tcgtctgccg gctctttgag ctgccacccc	120
cccaaacgag ccagcgagcg agcgaacgcg acagggggga gagtgccca	168

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<211> 8
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<213> Artificial Sequence

<220>
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synthetic construct

<400> 21
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8

<210> 22
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 22
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8

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 23
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21

ATTORNEY DOCKET NO. 14014.0323U3

<210> 24
 <211> 735
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 24

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Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
			20					25					30		
Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
		35					40					45			
Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
	50					55					60				
Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
65					70					75					80
Arg	Gln	Leu	Asp	Ser	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala
				85					90					95	
Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Lys	Glu	Asp	Thr	Ser	Phe	Gly	Gly
			100					105					110		
Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro
		115					120					125			
Leu	Gly	Leu	Val	Glu	Glu	Pro	Val	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg
	130					135					140				
Pro	Val	Glu	His	Ser	Pro	Val	Glu	Pro	Asp	Ser	Ser	Ser	Gly	Thr	Gly
145					150					155					160
Lys	Ala	Gly	Gln	Gln	Pro	Ala	Arg	Lys	Arg	Leu	Asn	Phe	Gly	Gln	Thr
				165					170					175	
Gly	Asp	Ala	Asp	Ser	Val	Pro	Asp	Pro	Gln	Pro	Leu	Gly	Gln	Pro	Pro
			180					185					190		
Ala	Ala	Pro	Ser	Gly	Leu	Gly	Thr	Asn	Thr	Met	Ala	Thr	Gly	Ser	Gly
		195					200					205			
Ala	Pro	Met	Ala	Asp	Asn	Asn	Glu	Gly	Ala	Asp	Gly	Val	Gly	Asn	Ser
	210					215					220				
Ser	Gly	Asn	Trp	His	Cys	Asp	Ser	Thr	Trp	Met	Gly	Asp	Arg	Val	Ile
225					230					235					240
Thr	Thr	Ser	Thr	Arg	Thr	Trp	Ala	Leu	Pro	Thr	Tyr	Asn	Asn	His	Leu
				245					250					255	
Tyr	Lys	Gln	Ile	Ser	Ser	Gln	Ser	Gly	Ala	Ser	Asn	Asp	Asn	His	Tyr
			260					265					270		
Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn	Arg	Phe	His
		275					280					285			
Cys	His	Phe	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn	Asn	Asn	Trp
	290					295					300				
Gly	Phe	Arg	Pro	Lys	Arg	Leu	Asn	Phe	Lys	Leu	Phe	Asn	Ile	Gln	Val
305					310					315					320
Lys	Glu	Val	Thr	Gln	Asn	Asp	Gly	Thr	Thr	Thr	Ile	Ala	Asn	Asn	Leu
				325					330					335	
Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	Asp	Ser	Glu	Tyr	Gln	Leu	Pro	Tyr
			340					345					350		
Val	Leu	Gly	Ser	Ala	His	Gln	Gly	Cys	Leu	Pro	Pro	Phe	Pro	Ala	Asp
		355					360					365			
Val	Phe	Met	Val	Pro	Gln	Tyr	Gly	Tyr	Leu	Thr	Leu	Asn	Asn	Gly	Ser
	370					375					380				
Gln	Ala	Val	Gly	Arg	Ser	Ser	Phe	Tyr	Cys	Leu	Glu	Tyr	Phe	Pro	Ser
385					390					395					400

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Gln	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Thr	Phe	Ser	Tyr	Thr	Phe	Glu
				405					410					415	
Asp	Val	Pro	Phe	His	Ser	Ser	Tyr	Ala	His	Ser	Gln	Ser	Leu	Asp	Arg
			420					425					430		
Leu	Met	Asn	Pro	Leu	Ile	Asp	Gln	Tyr	Leu	Tyr	Tyr	Leu	Ser	Arg	Thr
		435					440					445			
Asn	Thr	Pro	Ser	Gly	Thr	Thr	Thr	Gln	Ser	Arg	Leu	Gln	Phe	Ser	Gln
	450					455					460				
Ala	Gly	Ala	Ser	Asp	Ile	Arg	Asp	Gln	Ser	Arg	Asn	Trp	Leu	Pro	Gly
465					470					475					480
Pro	Cys	Tyr	Arg	Gln	Gln	Arg	Val	Ser	Lys	Thr	Ser	Ala	Asp	Asn	Asn
				485					490					495	
Asn	Ser	Glu	Tyr	Ser	Trp	Thr	Gly	Ala	Thr	Lys	Tyr	His	Leu	Asn	Gly
			500					505					510		
Arg	Asp	Ser	Leu	Val	Asn	Pro	Gly	Pro	Ala	Met	Ala	Ser	His	Lys	Asp
		515					520					525			
Asp	Glu	Glu	Lys	Phe	Phe	Pro	Gln	Ser	Gly	Val	Leu	Ile	Phe	Gly	Lys
	530					535					540				
Gln	Gly	Ser	Glu	Lys	Thr	Asn	Val	Asp	Ile	Glu	Lys	Val	Met	Ile	Thr
545					550					555					560
Asp	Glu	Glu	Glu	Ile	Arg	Thr	Thr	Asn	Pro	Val	Ala	Thr	Glu	Gln	Tyr
				565					570					575	
Gly	Ser	Val	Ser	Thr	Asn	Leu	Gln	Arg	Gly	Asn	Arg	Gln	Ala	Ala	Thr
			580					585					590		
Ala	Asp	Val	Asn	Thr	Gln	Gly	Val	Leu	Pro	Gly	Met	Val	Trp	Gln	Asp
		595					600					605			
Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	His	Thr
	610					615					620				
Asp	Gly	His	Phe	His	Pro	Ser	Pro	Leu	Met	Gly	Gly	Phe	Gly	Leu	Lys
625					630					635					640
His	Pro	Pro	Pro	Gln	Ile	Leu	Ile	Lys	Asn	Thr	Pro	Val	Pro	Ala	Asn
				645					650					655	
Pro	Ser	Thr	Thr	Phe	Ser	Ala	Ala	Lys	Phe	Ala	Ser	Phe	Ile	Thr	Gln
			660					665					670		
Tyr	Ser	Thr	Gly	Gln	Val	Ser	Val	Glu	Ile	Glu	Trp	Glu	Leu	Gln	Lys
		675					680					685			
Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Ser	Asn	Tyr
	690					695					700				
Asn	Lys	Ser	Val	Asn	Val	Asp	Phe	Thr	Val	Asp	Thr	Asn	Gly	Val	Tyr
705					710					715					720
Ser	Glu	Pro	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu	Thr	Arg	Asn	Leu	
				725					730					735	

C1
cancel